Amendments to the Claims

Please amend Claims 1 and 11. Please add new Claim 19. The Claim Listing below will replace all prior versions of the claims in the application.

Claim Listing

1.   (Currently amended) In a computer system, a method for clustering a plurality of datapoints, wherein each datapoint is a series of gene expression values, wherein the method comprises:

   a)   receiving the gene expression values of the datapoints;

   b)   using a self organizing map, clustering the datapoints such that the datapoints that exhibit similar patterns are clustered together into respective clusters, wherein prior knowledge of the datapoints to be clustered [in] is not necessary; and

   c)   providing an output indicating the clusters of the datapoints.

2.   (Original) The method of Claim 1, wherein the gene expression values are obtained from a gene that is subjected to at least one condition.

3.   (Original) The method of Claim 2, the step of receiving includes receiving gene expression values of datasets, wherein a dataset is a series of gene expression values across multiple genes for a condition.

4.   (Original) The method of Claim 3, further comprising filtering out any datapoints that exhibit an insignificant change in the gene expression value, such that working datapoints remain.

5.   (Original) The method of Claim 4, further comprising normalizing the gene expression value of the working datapoints.

6. (Original) The method of Claim 5, wherein the self organizing map is formed of a plurality of Nodes, N, and clusters the datapoints according to a competitive learning routine.

7. (Original) The method of Claim 6, wherein the competitive learning routine is:

$$f_{i+1}(N) = f_i(N) + \tau(d(N,N_P), i) (P - f_i(N))$$

wherein i = number of iterations, N= the node of the self organizing map, τ = learning rate, P = the subject working datapoint, d = distance, N_p = node that is mapped nearest to P, and $f_i(N)$ is the position of N at i.

8. (Original) The method of Claim 1, wherein the step of providing includes displaying at least one representative datapoint from each cluster.

9. (Original) The method of Claim 5, wherein the step of normalizing the gene expression value comprises determining the ratio of a) difference between the subject gene expression value and the average gene expression value across datasets, and b) the standard deviation of the gene expression value across datasets.

10. (Original) The method of Claim 3, further comprising rescaling the gene expression values to account for variations across multiple conditions.

11. (Currently amended) In a computer system, a method for grouping a plurality of datapoints, wherein each datapoint is a series of gene expression values, wherein the method comprises:
    a)   receiving gene expression values of the datapoints;
    b)   filtering out any datapoints that exhibit an insignificant change in the gene expression value, such that working datapoints remain;
    c)   normalizing the gene expression value of the working datapoints;

d)   using a self organizing map, grouping the working datapoints such that the datapoints that exhibit similar patterns are grouped together into respective clusters, wherein prior knowledge of the datapoints to be clustered [in] is not necessary; and

e)   providing an output indicating the groups of the datapoints.

12.   (Original) The method of Claim 11, wherein the gene expression values are obtained from a gene that is subjected to at least one condition.

13.   (Original) The method of Claim 12, the step of receiving includes receiving gene expression values of datasets, wherein a dataset is a series of gene expression values across multiple genes for a condition.

14.   (Original) The method of Claim 13, wherein the self organizing map is formed of a plurality of Nodes, N, and groups the datapoints according to a competitive learning routine.

15.   (Original) The method of Claim 14, wherein the competitive learning routine is:

$$f_{i+1}(N) = f_i(N) + \tau(d(N,N_P), i) (P - f_i(N))$$

wherein i = number of iterations, N = the node of the self organizing map, τ = learning rate, P = the subject working datapoint, d = distance, N_p = node that is mapped nearest to P, and $f_i(N)$ is the position of N at i.

16.   (Original) The method of Claim 11, wherein the step of providing includes displaying at least one representative datapoint from each group.

17.   (Original) The method of Claim 13, wherein the step of normalizing the gene expression value comprises determining the ratio of a) difference between the subject gene

expression value and the average gene expression value across datasets, and b) the standard deviation of the gene expression value across datasets.

18.   (Original) The method of Claim 11, further comprising rescaling the gene expression values to account for variations across multiple conditions.

19.   (New) In a computer system, a method for clustering a plurality of datapoints, wherein each datapoint is a series of gene expression values, wherein the method comprises:

a)   receiving the gene expression values of the datapoints;

b)   using a self organizing map, clustering the datapoints such that the datapoints that exhibit similar patterns are clustered together into respective clusters, wherein prior knowledge of the datapoints to be clustered is not necessary; and

c)   providing an output indicating the clusters of the datapoints,

including displaying at least one representative datapoint from each cluster.